

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/978,891B

DATE: 05/27/93
TIME: 16:26:24
S4547

LINE ORIGINAL TEXT

CORRECTED TEXT

14 (iv) CORRESPONDING ADDRESS:
344 (3) INFORMATION FOR SEQ ID NO: 2:
670 (4) INFORMATION FOR SEQ ID NO: 3:
688 (5) INFORMATION FOR SEQ ID NO: 4:
705 (6) INFORMATION FOR SEQ ID NO: 5:
740 (7) INFORMATION FOR SEQ ID NO: 6:
759 (8) INFORMATION FOR SEQ ID NO: 7:
778 (9) INFORMATION FOR SEQ ID NO: 8:

(iv) CORRESPONDENCE ADDRESS:
(2) INFORMATION FOR SEQ ID NO: 2:
(2) INFORMATION FOR SEQ ID NO: 3:
(2) INFORMATION FOR SEQ ID NO: 4:
(2) INFORMATION FOR SEQ ID NO: 5:
(2) INFORMATION FOR SEQ ID NO: 6:
(2) INFORMATION FOR SEQ ID NO: 7:
(2) INFORMATION FOR SEQ ID NO: 8:

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/978,891B

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S4547

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/978,891B

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DATE: 05/27/93

TIME: 16:26:24

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LINE ERROR

ORIGINAL TEXT

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05/27/93
16:24:59
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Patent Application US/07/978,891B

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Darrell Anderson, Nabil Hanna, John Leonard,
Roland Newman and Mitchell Reff

(ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC
ANTIBODY TO HUMAN B LYMPHOCYTE

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDING ADDRESS:

(A) ADDRESSEE: IDEC Pharmaceuticals Corporation
(B) STREET: 11099 N. Torrey Pines Road, #160
(C) CITY: La Jolla
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
(B) COMPUTER: Macintosh
(C) OPERATING SYSTEM: MS.DOS
(D) SOFTWARE: Microsoft Word 5.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/07/978,891B
(B) FILING DATE: 13 NOV 1992
(C) CLASSIFICATION: 424

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Burgoon, Richard P. Jr.
(B) REGISTRATION NUMBER: 34,787
(C) REFERENCE/DOCKET NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 458-0600
(B) TELEFAX: (619) 546-9274

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8540 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: no

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(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9209 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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441	ATGGGTTGGA	GCCTCATCTT	GCTCTTCCTT	GTCGCTGTTG	CTACGCGTGT	CCTGTCCCAG	2460
442							
443	GTACAACTGC	AGCAGCCTGG	GGCTGAGCTG	GTGAAGCCTG	GGGCCTCAGT	GAAGATGTCC	2520
444							
445	TGCAAGGCTT	CTGGCTACAC	ATTTACCAGT	TACAATATGC	ACTGGGTAAA	ACAGACACCT	2580
446							
447	GGTCGGGGCC	TGGAATGGAT	TGGAGCTATT	TATCCCGGAA	ATGGTGATAC	TTCCTACAAT	2640
448							
449	CAGAAGTTCA	AAGGCAAGGC	CACATTGACT	GCAGACAAAT	CCTCCAGCAC	AGCCTACATG	2700
450							
451	CAGCTCAGCA	GCCTGACATC	TGAGGACTCT	GCGGTCTATT	ACTGTGCAAG	ATCGACTTAC	2760
452							
453	TACGGCGGTG	ACTGGTACTT	CAATGTCTGG	GGCGCAGGGA	CCACGGTCAC	CGTCTCTGCA	2820
454							
455	GCTAGCACCA	AGGGCCCATC	GGTCTTCCCC	CTGGCACCCCT	CCTCCAAGAG	CACCTCTGGG	2880
456							
457	GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGGTGTCG	2940
458							
459	TGGAATCAG	GCGCCCTGAC	CAGCGGCGTG	CACACCTTCC	CGGCTGTCCT	ACAGTCCTCA	3000
460							
461	GGAATCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC	3060
462							
463	TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGCAGAGCCC	3120
464							
465	AAATCTTG TG	ACAAAATCA	CACATGCCCA	CCGTGCCCAG	CACCTGAACT	CCTGGGGGGA	3180
466							
467	CCGTCAGTCT	TCCTCTTCCC	CCCAAAACCC	AAGGACACCC	TCATGATCTC	CCGGACCCCT	3240
468							

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469	GAGGTCACAT	GCGTGGTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	3300
470							
471	TACGTGGACG	GCGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGCGGGAGGA	GCAGTACAAC	3360
472							
473	AGCACGTACC	GTGTGGTCAG	CGTCCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	3420
474							
475	GAGTACAAGT	GCAAGGTCTC	CAACAAAGCC	CTCCCAGCCC	CCATCGAGAA	AACCATCTCC	3480
476							
477	AAAGCCAAAG	GGCAGCCCCG	AGAACCACAG	GTGTACACCC	TGCCCCCATC	CCGGGATGAG	3540
478							
479	CTGACCAAGA	ACCAGGTCAG	CCTGACCTGC	CTGGTCAAAG	GCTTCTATCC	CAGCGACATC	3600
480							
481	GCCGTGGAGT	GGGAGAGCAA	TGGGCAGCCG	GAGAACAAC	ACAAGACCAC	GCCTCCCGTG	3660
482							
483	CTGGACTCCG	ACGGCTCCTT	CTTCCTCTAC	AGCAAGCTCA	CCGTGGACAA	GAGCAGGTGG	3720
484							
485	CAGCAGGGGA	ACGTCTTCTC	ATGCTCCGTG	ATGCATGAGG	CTCTGCACAA	CCACTACACG	3780
486							
487	CAGAAGAGCC	TCTCCCTGTC	TCCGGGTAAA	TGAGGATCCG	TTAACGGTTA	CCAACTACCT	3840
488							
489	AGACTGGATT	CGTGACAACA	TGCGGCCGTG	ATATCTACGT	ATGATCAGCC	TCGACTGTGC	3900
490							
491	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	3960
492							
493	GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	4020
494							
495	GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	4080
496							
497	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGA	ACCAGCTGGG	GCTCGACAGC	4140
498							
499	GCTGGATCTC	CCGATCCCCA	GCTTTGCTTC	TCAATTTCTT	ATTTGCATAA	TGAGAAAAAA	4200
500							
501	AGGAAAATTA	ATTTTAACAC	CAATTCAGTA	GTTGATTGAG	CAAATGCGTT	GCCAAAAAGG	4260
502							
503	ATGCTTTAGA	GACAGTGTTT	TCTGCACAGA	TAAGGACAAA	CATTATTCAG	AGGGAGTACC	4320
504							
505	CAGAGCTGAG	ACTCCTAAGC	CAGTGAGTGG	CACAGCATTC	TAGGGAGAAA	TATGCTTGTC	4380
506							
507	ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGTAAAG	GGCCAATCTG	CTCACACAGG	4440
508							
509	ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
510							
511	CATTTGCTTC	TGACATAGTT	GTGTTGGGAG	CTTGATAGC	TTGGACAGCT	CAGGGCTGCG	4560
512							
513	ATTTGCGGCC	AAACTTGACG	GCAATCCTAG	CGTGAAGGCT	GGTAGGATTT	TATCCCCGCT	4620
514							
515	GCCATCATGG	TTCGACCATT	GAACTGCATC	GTCGCCGTGT	CCCAAAATAT	GGGGATTGGC	4680
516							
517	AAGAACGGAG	ACCTACCCTG	GCCTCCGCTC	AGGAACGAGT	TCAAGTACTT	CCAAAGAATG	4740
518							
519	ACCACAACCT	CTTCAGTGGA	AGGTAAACAG	AATCTGGTGA	TTATGGGTAG	GAAAACCTGG	4800
520							

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521	TTCTCCATTC	CTGAGAAGAA	TCGACCTTTA	AAGGACAGAA	TTAATATAGT	TCTCAGTAGA	4860
522							
523	GAAGTCAAAG	AACCACCACG	AGGAGCTCAT	TTTCTTGCCA	AAAGTTTGGA	TGATGCCTTA	4920
524							
525	AGACTTATTG	AACAACCGGA	ATTGGCAAGT	AAAGTAGACA	TGGTTTGGAT	AGTCGGAGGC	4980
526							
527	AGTTCTGTTT	ACCAGGAAGC	CATGAATCAA	CCAGGCCACC	TTAGACTCTT	TGTGACAAGG	5040
528							
529	ATCATGCAGG	AATTTGAAAG	TGACACGTTT	TTCCAGAAA	TTGATTTGGG	GAAATATAAA	5100
530							
531	CTTCTCCCAG	AATACCCAGG	CGTCCTCTCT	GAGGTCCAGG	AGGAAAAGG	CATCAAGTAT	5160
532							
533	AAGTTTGAAG	TCTACGAGAA	GAAAGACTAA	CAGGAAGATG	CTTTCAAGTT	CTCTGCTCCC	5220
534							
535	CTCCTAAAGC	TATGCATTTT	TATAAGACCA	TGGGACTTTT	GCTGGCTTTA	GATCAGCCTC	5280
536							
537	GACTGTGCCT	TCTAGTTGCC	AGCCATCTGT	TGTTTGCCCC	TCCCCCGTGC	CTTCCTTGAC	5340
538							
539	CCTGGAAGGT	GCCACTCCCA	CTGTCCTTTC	CTAATAAAAT	GAGGAAATTG	CATCGCATTG	5400
540							
541	TCTGAGTAGG	TGTCATTCTA	TTCTGGGGGG	TGGGGTGGGG	CAGGACAGCA	AGGGGGAGGA	5460
542							
543	TTGGGAAGAC	AATAGCAGGC	ATGCTGGGGA	TGCGGTGGGC	TCTATGGAAC	CAGCTGGGGC	5520
544							
545	TCGAGCTACT	AGCTTTGCTT	CTCAATTTCT	TATTTGCATA	ATGAGAAAAA	AAGGAAAATT	5580
546							
547	AATTTTAACA	CCAATTCAGT	AGTTGATTGA	GCAAATGCGT	TGCCAAAAG	GATGCTTTAG	5640
548							
549	AGACAGTGTT	CTCTGCACAG	ATAAGGACAA	ACATTATTCA	GAGGGAGTAC	CCAGAGCTGA	5700
550							
551	GACTCCTAAG	CCAGTGAGTG	GCACAGCATT	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	5760
552							
553	GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	5820
554							
555	GCAGGAGCCA	GGGCAGAGCA	TATAAGGTGA	GGTAGGATCA	GTTGCTCCTC	ACATTTGCTT	5880
556							
557	CTGACATAGT	TGTGTTGGGA	GCTTGGATCG	ATCCTCTATG	GTTGAACAAG	ATGGATTGCA	5940
558							
559	CGCAGGTTCT	CCGGCCGCTT	GGGTGGAGAG	GCTATTCGGC	TATGACTGGG	CACAACAGAC	6000
560							
561	AATCGGCTGC	TCTGATGCCG	CCGTGTTCCG	GCTGTCAGCG	CAGGGGCGCC	CGGTTCTTTT	6060
562							
563	TGTCAAGACC	GACCTGTCCG	GTGCCCTGAA	TGAACTGCAG	GACGAGGCAG	CGCGGCTATC	6120
564							
565	GTGGCTGGCC	ACGACGGGCG	TTCCTTGCGC	AGCTGTGCTC	GACGTTGTCA	CTGAAGCGGG	6180
566							
567	AAGGGACTGG	CTGCTATTGG	GCGAAGTGCC	GGGGCAGGAT	CTCCTGTCAT	CTCACCTTGC	6240
568							
569	TCCTGCCGAG	AAAGTATCCA	TCATGGCTGA	TGCAATGCGG	CGGCTGCATA	CGCTTGATCC	6300
570							
571	GGCTACCTGC	CCATTGCACC	ACCAAGCGAA	ACATCGCATC	GAGCGAGCAC	GTAATCGGAT	6360
572							

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573	GGAAGCCGGT	CTTGTCGATC	AGGATGATCT	GGACGAAGAG	CATCAGGGGC	TCGCGCCAGC	6420
574							
575	CGAACTGTTC	GCCAGGCTCA	AGGCGCGCAT	GCCCCACGGC	GAGGATCTCG	TCGTGACCCA	6480
576							
577	TGGCGATGCC	TGCTTGCCGA	ATATCATGGT	GGAAAATGGC	CGCTTTTCTG	GATTCATCGA	6540
578							
579	CTGTGGCCGG	CTGGGTGTGG	CGGACCGCTA	TCAGGACATA	GCGTTGGCTA	CCCGTGATAT	6600
580							
581	TGCTGAAGAG	CTTGCGGGCG	AATGGGCTGA	CCGCTTCCTC	GTGCTTTACG	GTATCGCCGC	6660
582							
583	TCCCGATTCT	CAGCGCATCG	CCTTCTATCG	CCTTCTTGAC	GAGTTCTTCT	GAGCGGGACT	6720
584							
585	CTGGGGTTCT	AAATGACCGA	CCAAGCGACG	CCCAACCTGC	CATCACGAGA	TTTCGATTCC	6780
586							
587	ACCGCCGCCT	TCTATGAAAG	GTTGGGCTTC	GGAATCGTTT	TCCGGGACGC	CGGCTGGATG	6840
588							
589	ATCCTCCAGC	GCGGGGATCT	CATGCTGGAG	TTCTTCGCCC	ACCCCAACTT	GTTTATTGCA	6900
590							
591	GCTTATAATG	GTTACAAATA	AAGCAATAGC	ATCACAAATT	TCACAAATAA	AGCATTTTTT	6960
592							
593	TCACTGCATT	CTAGTTGTGG	TTTGTCCAAA	CTCATCAATC	TATCTTATCA	TGTCTGGATC	7020
594							
595	GCGGCCGCGA	TCCCGTCGAG	AGCTTGGCGT	AATCATGGTC	ATAGCTGTTT	CCTGTGTGAA	7080
596							
597	ATTGTTATCC	GCTCACAATT	CCACACAACA	TACGAGCCGG	AAGCATAAAG	TGTAAAGCCT	7140
598							
599	GGGGTGCCTA	ATGAGTGAGC	TAACTCACAT	TAATTGCGTT	GCGCTCACTG	CCCGCTTTCC	7200
600							
601	AGTCGGGAAA	CCTGTCGTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	7260
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603	GTTTGCGTAT	TGGGCGCTCT	TCCGCTTCCT	CGCTCACTGA	CTCGCTGCGC	TCGGTCGTTC	7320
604							
605	GGCTGCGGCG	AGCGGTATCA	GCTCACTCAA	AGGCGGTAAT	ACGGTTATCC	ACAGAATCAG	7380
606							
607	GGGATAACGC	AGGAAAGAAC	ATGTGAGCAA	AAGGCCAGCA	AAAGGCCAGG	AACCGTAAAA	7440
608							
609	AGGCCGCGTT	GCTGGCGTTT	TTCCATAGGC	TCCGCCCCCC	TGACGAGCAT	CACAAAAATC	7500
610							
611	GACGCTCAAG	TCAGAGGTGG	CGAAACCCGA	CAGGACTATA	AAGATACCAG	GCGTTTCCCC	7560
612							
613	CTGGAAGCTC	CCTCGTGCGC	TCTCCTGTTC	CGACCCTGCC	GCTTACCGGA	TACCTGTCCG	7620
614							
615	CCTTTCTCCC	TTCGGGAAGC	GTGGCGCTTT	CTCAATGCTC	ACGCTGTAGG	TATCTCAGTT	7680
616							
617	CGGTGTAGGT	CGTTCGCTCC	AAGCTGGGCT	GTGTGCACGA	ACCCCCGTT	CAGCCCGACC	7740
618							
619	GCTGCGCCTT	ATCCGGTAAC	TATCGTCTTG	AGTCCAACCC	GGTAAGACAC	GACTTATCGC	7800
620							
621	CACTGGCAGC	AGCCACTGGT	AACAGGATTA	GCAGAGCGAG	GTATGTAGGC	GGTGCTACAG	7860
622							
623	AGTTCTTGAA	GTGGTGGCCT	AACTACGGCT	ACACTAGAAG	GACAGTATTT	GGTATCTGCG	7920
624							

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625	CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAAACAAA	7980
626		
627	CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAG	8040
628		
629	GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT	8100
630		
631	CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAGGAT CTTACCTAG ATCCTTTTAA	8160
632		
633	ATTAAAAATG AAGTTTTTAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT	8220
634		
635	ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG	8280
636		
637	TTGCCTGACT CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA	8340
638		
639	GTGCTGCAAT GATACGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC	8400
640		
641	AGCCAGCCGG AAGGGCCGAG CGCAGAAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT	8460
642		
643	CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG	8520
644		
645	TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA	8580
646		
647	GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG	8640
648		
649	TTAGCTCCTT CGGTCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA	8700
650		
651	TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG	8760
652		
653	TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT	8820
654		
655	CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA	8880
656		
657	TCATTGAAA ACGTTCTTCG GGGCGAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA	8940
658		
659	GTTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG	9000
660		
661	TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC	9060
662		
663	GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT	9120
664		
665	ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC	9180
666		
667	CGCGCACATT TCCCCGAAAA GTGCCACCT	9209
668		
669		

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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677 (ii) MOLECULE TYPE: DNA (genomic)
678
679 (iii) HYPOTHETICAL: no
680
681 (iv) ANTI-SENSE: no
682
683 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
684
685 ATC ACA GAT CTC TCA CCA TGG ATT TTC AGG TBC AGA TTA TCA GCT 45
686 TC 47
687
688 (5) INFORMATION FOR SEQ ID NO: 4:
689 (i) SEQUENCE CHARACTERISTICS:
690 (A) LENGTH: 30 bases
691 (B) TYPE: nucleic acid
692 (C) STRANDEDNESS: single
693 (D) TOPOLOGY: linear
694
695 (ii) MOLECULE TYPE: DNA (genomic)
696
697 (iii) HYPOTHETICAL: no
698
699 (iv) ANTI-SENSE: yes
700
701 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
702
703 TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 30
704
705 (6) INFORMATION FOR SEQ ID NO: 5:
706
707 (i) SEQUENCE CHARACTERISTICS:
708
709 (A) LENGTH: 384 bases
710 (B) TYPE: nucleic acid
711 (C) STRANDEDNESS: single
712 (D) TOPOLOGY: linear
713
714 (ii) MOLECULE TYPE: DNA (genomic)
715
716 (iii) HYPOTHETICAL: no
717
718 (iv) ANTI-SENSE: no
719
720 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
721
722
723 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC 51
724
725 ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT 102
726
727 GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA 153
728

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729 AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG 204
730
731 ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC 255
732
733 AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA 306
734
735 GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG ACT AGT AAC CCA CCC ACG TTC 357
736
737 GGA GGG GGG ACC AAG CTG GAA ATC AAA 384
738

739
740 (7) INFORMATION FOR SEQ ID NO: 6:
741
742 (i) SEQUENCE CHARACTERISTICS:
743
744 (A) LENGTH: 27 bases
745 (B) TYPE: nucleic acid
746 (C) STRANDEDNESS: single
747 (D) TOPOLOGY: linear
748
749 (ii) MOLECULE TYPE: DNA (genomic)
750
751 (iii) HYPOTHETICAL: no
752
753 (iv) ANTI-SENSE: no
754
755 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
756
757 GCG GCT CCC ACG CGT GTC CTG TCC CAG 27
758

759 (8) INFORMATION FOR SEQ ID NO: 7:
760
761 (i) SEQUENCE CHARACTERISTICS:
762
763 (A) LENGTH: 29 bases
764 (B) TYPE: nucleic acid
765 (C) STRANDEDNESS: single
766 (D) TOPOLOGY: linear
767
768 (ii) MOLECULE TYPE: DNA (genomic)
769
770 (iii) HYPOTHETICAL: no
771
772 (iv) ANTI-SENSE: yes
773
774 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
775
776 GGS TGT TGT GCT AGC TGM RGA GAC RGT GA 29
777

778 (9) INFORMATION FOR SEQ ID NO: 8:
779
780 (i) SEQUENCE CHARACTERISTICS:

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781
782 (A) LENGTH: 420 bases
783 (B) TYPE: nucleic acid
784 (C) STRANDEDNESS: single
785 (D) TOPOLOGY: linear
786
787 (ii) MOLECULE TYPE: DNA (genomic)
788
789 (iii) HYPOTHETICAL: no
790
791 (iv) ANTI-SENSE: no
792
793 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
794
795 ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC 51
796
797 CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG 102
798
799 GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC 153
800
801 AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA 204
802
803 GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC 255
804
805 AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAG CTC 306
806
807 AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT GCA AGA TCG ACT 357
808
809 TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC GCA GGG ACC ACG GTC 408
810 ACC GTC TCT GCA 420
811